

# Molecular genetic analysis of *Varroa destructor* mites in brood, fallen injured mites and worker bee longevity in honey bees

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Identification of genes and markers associated with economically important traits will improve the efficiency of selective breeding efforts.

We tested for the presence of single nucleotide polymorphisms (SNPs) which associate with four traits.

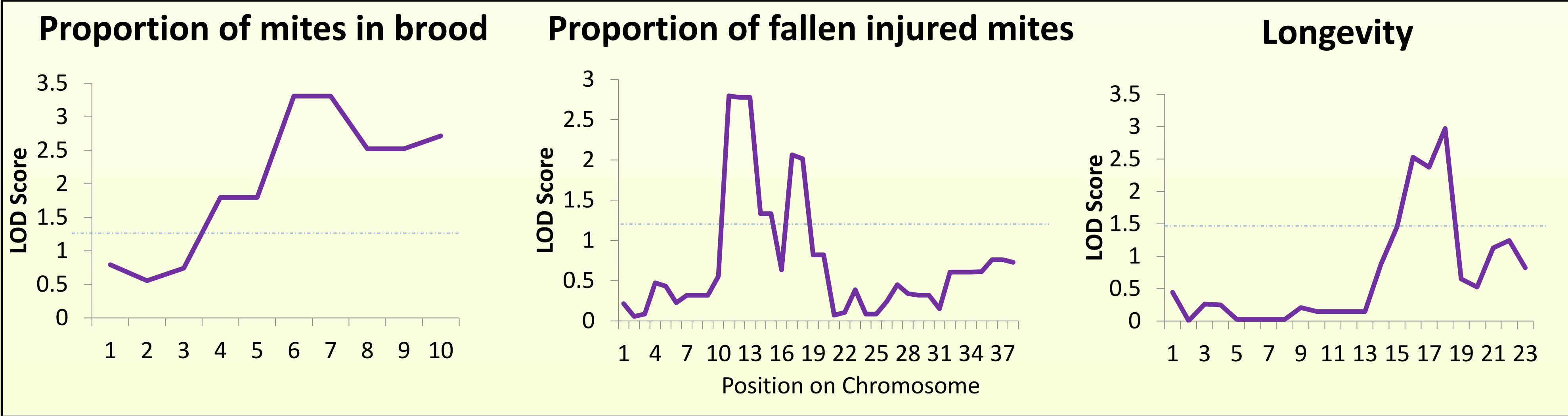
- Proportion of mites in the brood (MIB)
- Proportion of fallen injured mites (FIM)
- Longevity of worker bees

All of these traits have either known or potential associations to colony survival in a backcrossed Russian honey bee population.

## Approach

**Short-term goal:** Identify regions in the genome and potential markers within those regions that are associated with the four traits studied.

**Long term goal:** Develop marker-assisted selection for the traits that show the highest potential for stock improvement.



Putative Cellular Function	Number of Genes Within Interval		
	Mites in Brood	Fallen Injured Mites	Longevity
Apoptosis	0	4	0
Biological regulation	2	0	6
Biosynthesis	4	0	0
Cell metabolism	4	2	1
Cell proliferation	1	3	0
Cell regulation	13	25	12
Cell repair	0	1	0
Developmental	1	7	1
Immunological, cellular response	0	3	0
Longevity	1	0	1
Memory	3	0	0
Morphological	0	1	1
Motor function	0	3	1
Neurogenesis, neural signaling	5	16	3
Reproduction	2	0	1
Response to gravity	0	1	0
Sensory	2	1	0

## Results

Parameter	Mean ± SE
Colony and infestation parameters (n = 58 colonies)	
Number of capped worker brood	3,648.6 ± 344.1
Number of adult bees	5,496.8 ± 414.8
Number of mites in worker brood	306.8 ± 43.5
Number of mites in drone brood	8.6 ± 5.1
Number of mites on adult bees	208.3 ± 31.2
Total colony mites	315.4 ± 45.0
Percentage of mites in brood	54.0 ± 3.0
Mite drop parameters (n = 53 colonies)	
Total trapped mites	28.4 ± 1.7
Number of uninjured mites	22.8 ± 1.5
Number of injured mites	5.6 ± 0.3
Longevity parameters (n = 51 colonies)	
Days to 50% bees remaining	15.4 ± 0.6

Investigation of multiple traits in a single QTL study revealed a suite of genes that are potential candidates for further development.

## Conclusions

These genes, if their relevance remains high after validation studies, could be used in marker development for MAS in honey bees to improve colony survival through improving resistance to *Varroa* mites as well as worker longevity



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